

Wed Apr 16 08:08:22 2003

us-09-001-737-8.rsp

Page 1

GenCore version 5.1.4.ps_4578
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OM protein - protein search, using sw model

Run on: April 8, 2003, 14:23:17 : Search time 14 Seconds
(without alignments)
1614.614 Million cell updates/sec

Title: US-09-001-737-8
Perfect score: 2663
Sequence: 1 MAKEIKFSADRAAMVRCVD.....TPAPAMPAGMDPMGMGMG 545

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2638	99.4	542	1	CH60_STREY
2	2195.5	82.4	542	1	CH60_LACIA
3	2032.5	76.4	542	1	CH60_LISNO
4	2028.5	76.1	539	1	CH60_BAGST
5	2028.5	76.1	542	1	CH60_LISTN
6	2021.5	75.9	543	1	CH60_BACSD
7	2017.5	75.8	544	1	CH60_BACSD
8	1981	74.4	538	1	CH60_BACSD
9	1877.5	70.5	540	1	CH60_BACSD
10	1857.5	69.8	538	1	CH60_BACSD
11	1842.5	69.2	538	1	CH60_BACSD
12	1833.5	68.9	540	1	CH60_BACSD
13	1818	68.3	539	1	CH60_BACSD
14	1776	66.7	543	1	CH60_BACSD
15	1723.5	64.7	540	1	CH60_BACSD
16	1697	63.7	542	1	CH60_BACSD
17	1697	63.7	540	1	CH60_BACSD
18	1688.5	63.4	545	1	CH60_BACSD
19	1678.5	62.9	545	1	CH60_BACSD
20	1672.5	62.7	545	1	CH60_BACSD
21	1670.5	62.7	545	1	CH60_BACSD
22	1670.5	62.7	545	1	CH60_BACSD
23	1663.5	62.4	544	1	CH60_BACSD
24	1661.5	62.4	544	1	CH60_BACSD
25	1660	62.3	546	1	CH60_BACSD
26	1657.5	62.2	545	1	CH60_BACSD
27	1656	62.2	546	1	CH60_BACSD
28	1656	62.2	547	1	CH60_BACSD
29	1654	62.1	544	1	CH60_BACSD
30	1653	62.0	547	1	CH60_BACSD
31	1651	61.8	547	1	CH60_BACSD
32	1646	61.8	539	1	CH60_BACSD
33	1646	61.8	546	1	CH60_BACSD

34	1646	61.8	546	1	CH60_BACSD	P58723 burkholderi
35	1643	61.7	547	1	CH60_BACSD	P48210 bordetella
36	1642.5	61.7	539	1	CH60_BACSD	P06806 mycobacteri
37	1642	61.7	546	1	CH60_BACSD	Q92760 burkholderi
38	1642	61.7	546	1	CH60_BACSD	P42385 neisseria m
39	1641	61.6	539	1	CH60_BACSD	P77829 bradyrhizob
40	1640.5	61.6	547	1	CH60_BACSD	P06139 escherichia
41	1640	61.6	543	1	CH60_BACSD	Q57002 synechococc
42	1639	61.5	540	1	CH60_BACSD	O66212 klebsiella
43	1637	61.5	544	1	CH60_BACSD	P29842 neisseria g
44	1636	61.4	544	1	CH60_BACSD	Q9xau7 alteromonas
45	1635.5	61.4	547	1	CH60_BACSD	

ALIGNMENTS

RESULT 1
ID CH60_STREY STANDARD: PRT: 542 AA.
AC P82485;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 60 kDa chaperonin (protein Cpn60) (GroEL protein).
GN GROEL OR MOXA OR GROEL OR SPY2070.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP370 / ATCC 700294 / Serotype M1;
RX MEDLINE=1192684; PubMed=11296295;
RA Ferrerelli J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic S., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian X., Jia H.G., Najjar F.Z., Ren O., Zhu H., Song L., White J.,
RA Qian X., Clifton S.M., Roe B.A., McLaughlin R., Song L., White J.,
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RN [2]
RP PARTIAL SEQUENCE AND MASS SPECTROMETRY.
RC STRAIN=DJRS4 / Serotype M6;
RA Hogan D.A., Du P., Stevenson T.I., Whilton M., Kilby G.W., Rogers J.,
RA Vanbogaert R.A.;
RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
proteins.";
RL Submitted (MAY-2000) to the SWISS-PROT data bank.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CONDITIONS (BY SIMILARITY).
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC EMBL: AE006627; AAK34727.1;
CC HSSP: P06139; IGR1.
DR InterPro: IPR001844; Chaperin_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP-1.
DR Pfam: PF00118; Cpn60_TCP1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCP1.
DR PRINTS: PS00296; CHAPERONIN_CPN60.1.
DR Chaperone: Heat shock; ATP-binding; complete proteome.
FT INIT_MET 0
FT

SO SEQUENCE 542 AA: 56964 MW: C7B9A13B6FD71D4 CRC64:

Query Match 99.1%; Score 2638; DB 1; Length 542;
 Best Local Similarity 99.8%; Pred. No. 1,6e-114;
 Matches 540; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 AKEIKFSADARAAMRGVMDLADTVKVTIGPKGRNVVLEKAGSPFLITNDGVITAEIEI 61
 DB 1 AKDIKFSADARAAMRGVMDLADTVKVTIGPKGRNVVLEKAGSPFLITNDGVITAEIEI 60

OY 62 EDHFNMGAKLVSEVASKTNDIAGDGTATATVLOAIVHEGKANTGAMPDGRGIEI 121
 DB 61 EDHFNMGAKLVSEVASKTNDIAGDGTATATVLOAIVHEGKANTGAMPDGRGIEI 120

OY 122 ATATAVALKALIAQPVSGKEATNOVAASVSRSEKVEGYISEMERNVNDGVITIEESRG 181
 DB 121 ATATAVALKALIAQPVSGKEATNOVAASVSRSEKVEGYISEMERNVNDGVITIEESRG 180

OY 182 ETELEVEMGDFRGYSQYMTDNEKNVALEMPFLITDKKYSNIQDILPLEEVLT 241
 DB 181 ETELEVEMGDFRGYSQYMTDNEKNVALEMPFLITDKKYSNIQDILPLEEVLT 240

OY 242 NRPLLIADVDGEALPTLVNKIRGTNVAVAKAFGDRRKALMEDIALILGTGVITE 301
 DB 241 NRPLLIADVDGEALPTLVNKIRGTNVAVAKAFGDRRKALMEDIALILGTGVITE 300

OY 302 DLGLELKDATMTALGOAAKITVDKSTVIEGSGSSSEAIANRIALIKSOLETTSDPDR 361
 DB 301 DLGLELKDATMTALGOAAKITVDKSTVIEGSGSSSEAIANRIALIKSOLETTSDPDR 360

OY 362 KLOERLAKLAGVAIVKGAFTETALKEMKRIEDALNTRAAREEIVAGGTALITVI 421
 DB 361 KLOERLAKLAGVAIVKGAFTETALKEMKRIEDALNTRAAREEIVAGGTALITVI 420

OY 422 EKVAALEEGDDATGRNIVRLAEPVROIALNAGVSVYIDLKNSPAGTGFNAATG 481
 DB 421 EKVAALEEGDDATGRNIVRLAEPVROIALNAGVSVYIDLKNSPAGTGFNAATG 480

OY 482 WMDKITGTIIDPVKVTYSALQNAASVSLITTEAVVANKPEPATPAPAMPAMDPMGM 541
 DB 481 WMDKITGTIIDPVKVTYSALQNAASVSLITTEAVVANKPEPATPAPAMPAMDPMGM 540

OY 542 G 542

DB 541 G 541

RESULT 2

ID CH60_LACIA STANDARD: PRT: 542 AA.
 AC P37282;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 15-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).
 GN GROEL OR MOBA OR GROEL OR L10394.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria: Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93552268; PubMed=8486277;
 RA KIM S.G., BALT C.A.;
 RA "Cloning and sequencing of the Lactococcus lactis subsp. lactis
 RT groEL operon";
 RL Gene 127:121-126(1993).
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL1403;
 RC MEDLINE=2135186; PubMed=11337471;
 RA BOLTIN A., WINCKER P., MAUGER S., JAILLON O., MALARME K.,
 RA WEISENBACH J., EHRLICH S.D., SOROKIN A.;
 "The complete genome sequence of the lactic acid bacterium Lactococcus

RT Lactis ssp. lactis IL1403.*;
 RL Genome Res. 11:731-753(2001).
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
 CC CONDITIONS (BY SIMILARITY).
 CC SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
 CC 7 SUBUNITS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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DR EMBL: X71132; CAAS0446.1;
 DR EMBL: AE006276; AAK04492.1;
 DR PIR: S32106; S32106.
 DR PIR: JN0661; JN0661.
 DR HSSP: P06139; IGR.
 DR InterPro: IPR001844; Chaperonin_Cpn60.
 DR InterPro: IPR002423; Cpn60_TCP1.
 DR Pfam: PF00118; Cpn60_TCP1.1.
 DR PRINTS: PR00298; CHAPERONIN60.
 DR PRINTS: PR00304; TCOMPLEXTCP1.
 DR PROSITE: PS00296; CHAPERONIN_CPN60.1.
 KW Chaperone; ATP-binding; Complete proteome.
 KW CONFLICT 63
 FT CONFLICT 88 D -> V (IN REF. 1).
 FT CONFLICT 89 T -> N (IN REF. 1).
 FT CONFLICT 289 D -> H (IN REF. 1).
 FT CONFLICT 367 L -> V (IN REF. 1).
 FT CONFLICT 542 M -> I (IN REF. 1).
 SQ SEQUENCE 542 AA: 57201 MW: D7D6F5319DA59721 CRC64:

Query Match 82.4%; Score 2195.5; DB 1; Length 542;
 Best Local Similarity 81.1%; Pred. No. 3.2e-94;
 Matches 442; Conservative 52; Mismatches 46; Indels 5; Gaps 3;

OY 1 MAKEIKFSADARAAMRGVMDLADTVKVTIGPKGRNVVLEKAGSPFLITNDGVITAEIEI 60
 DB 1 MSKDIKFSADARAAMRGVMDLADTVKVTIGPKGRNVVLEKAGSPFLITNDGVITAEIEI 60

OY 61 LEDHFNMGAKLVSEVASKTNDIAGDGTATATVLOAIVHEGKANTGAMPDGRGIEI 120
 DB 61 LEDHFNMGAKLVSEVASKTNDIAGDGTATATVLOAIVHEGKANTGAMPDGRGIEI 120

OY 121 TATATAVALKALIAQPVSGKEATNOVAASVSRSEKVEGYISEMERNVNDGVITIEESRG 180
 DB 121 LAETAVASIKEMALPVHDKSAIQAYVSSRSKVEGYISDMERNVSDGVITIEESRG 180

OY 181 METELEVEMGDFRGYSQYMTDNEKNVALEMPFLITDKKYSNIQDILPLEEVLT 240
 DB 181 METELEVEMGDFRGYSQYMTDNEKNVALEMPFLITDKKYSNIQDILPLEEVLT 240

OY 241 TNRPLLIADVDGEALPTLVNKIRGTNVAVAKAFGDRRKALMEDIALILGTGVITE 300
 DB 241 TNRPLLIADVDGEALPTLVNKIRGTNVAVAKAFGDRRKALMEDIALILGTGVITE 300

OY 301 EDGLELKDATMTALGOAAKITVDKSTVIEGSGSSSEAIANRIALIKSOLETTSDPDR 360
 DB 301 BELGLDKDATLEAAGAAKATVDKHTTIEGAGSADATSDRAVIAIKOJKTSTSDPDR 360

OY 361 EKLDERLAKLAGVAIVKGAFTETALKEMKRIEDALNTRAAREEIVAGGTALITVI 420
 DB 361 EKLDERLAKLAGVAIVKGAFTETALKEMKRIEDALNTRAAREEIVAGGTALITVI 420

OY 421 EKVAALEEGDDATGRNIVRLAEPVROIALNAGVSVYIDLKNSPAGTGFNAATG 480
 DB 421 INALDKSESGDIQIGINIRVRLAEPVROIALNAGVSVYIDLKNSPAGTGFNAATG 480

OY 481 EMDKITGTIIDPVKVTYSALQNAASVSLITTEAVVANKPEPATPAPAMPAMDPMGM 540

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Db 481 QMVMIEGIVDPKATVRSALONNASSVALITTEAVANKPEPA--APAPP-KDPSPH- 536
QY 541 GKGCG 545
Db 537 -GKGCG 540

RESULT 3
CH60_LISMO STANDARD; PRT: 542 AA.
ID CH60_LISMO
AC 09AGE6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 60 kDa chaperonin (protein Cpn60) (groEL protein).
GN GROEL OR GROEL OR LMO2068.
OS Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;

RP SEQUENCE FROM N.A.
RC STRAIN-LO28 / Serovar 1/2c;
RX MEDLINE-21246697; PubMed-11349060;
RA Gahan C.G., O'Mahony J., Hill C.;
RT "Characterization of the groEL operon in Listeria monocytogenes:
RL utilization of two reporter systems (gfp and hly) for evaluating in
RN vivo expression."
RT Infect. Immun. 69:3924-3932(2001).
[2]

RP SEQUENCE FROM N.A.
RC STRAIN-EGD-e / Serovar 1/2a;
RX MEDLINE-21537279; PubMed-11679669;
RA Glaser P., Frangoul L., Buchliesser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetoui F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Desautget O.,
RA Entian K.-D., Fajhl H., Garcia-del Portillo F., Garrido P.,
RA Gautier L.-M., Kaerst U., Kreft J., Kuhn M., Kuntz F., Kurapkak G.,
RA Jones L., Goebel W., Gomez-Lopez N., Hain T., Hain J., Jackson D.,
RA Madueno E., Maitounan A., Mata Vicente J., Ng E., Niedlari H.,
RA Nordstedt G., Novella S., de Padlos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tietze A.,
RA Varquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
RL "Comparative genomics of Listeria species."
RT Science 294:849-852(2001).

-1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC -1- 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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DR EMBL: AF333323; AK28538.1;
DR EMBL: AL591982; CAD00146.1;
DR HSSP: P06139; GRL;
DR Listeria; LMO2068;
DR Interpro: IPR001844; Chaperonin.Cpn60.
DR Interpro: IPR002423; Cpn60/TCP-1.
DR Pfam: PF00118; Cpn60/TCP-1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONIN5.CPN60.1.
DR Chaperone; ATP-binding; Complete proteome.
KW Chaperone; ATP-binding; Complete proteome.
SQ SEQUENCE 542 AA; 57367 MW; 981845967D92944 CRC64;

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Query Match 76.4%; Score 2033.5; DB 1; Length 542;
Best Local Similarity 75.6%; Pred. No. 8.5e-87;
Matches 412; Conservative 61; Mismatches 67; Indels 5; Gaps 3;

QY 1 MAKEIFESADARAAMVAGVMDLADTVVLTGPGKRVVLEKAFGSPPLINDGVITAKEIE 60
DB 1 MAKDIFESDARRAMRGVDLANVYVLTGPGKRVVLEKKGSPPLINDGVITAKEIE 60
QY 61 LEDPFENNGAKVSEVASKTNDIAGDGTATATVLAQVHBDGKNTAGANPIGRGIE 120
DB 61 LEDPFENNGAKVSEVASKTNDVAGDGTATATVLAQVHBDGKNTAGANPVGRRGIE 120
QY 121 TATATPVALKATAIQPVSKREIAQVAAVSSEKVEYISEAMERYGNDGVITIEESRG 180
DB 121 KAVATRIEELKATSKPIESKESIAQVAAISSGDEEYGLIAEMERVGNDGVITIEESRG 180
QY 181 METELEVEGQEDRGYISQYVWTDNEKNVADLENPFILITDKKVSINDILPLEEVK 240
DB 181 FATELDVVEGQEDRGYISQYVWTDSDKMEAVLEKPYLITDKKINNIOEILPVLQVVO 240
QY 241 TNRPLLIADVDGALPTVLNKRGTFFNVVAVAPGCDRRKAMLEDIALLGTGVT 300
DB 241 QGRPHLIADVEDEGAQATVLNKRGTFFNVVAVAPGCDRRKAMLEDIALLGTGCVIT 300
QY 301 EDGLLELDATMTALGAAKITVDKSTVVEGSSSAIANRLAIKLSQLETTSPDFOR 360
DB 301 EDGLLELDATMTALGAAKITVDKSTVVEGSSSAIANRLAIKLSQLETTSPDFOR 360
QY 361 EKLQERLAKLAGVAVIKYGAFTETALKEMKLRIDALNTPRAVEGIVAGGTALITY 420
DB 361 EKLQERLAKLAGVAVIKYGAFTETALKEMKLRIDALNTPRAVEGIVAGGTALITY 420
QY 421 IEVVALELEDGATGRNIVLALEEPYQIALNNGVSGVYIDKKSPAGTGFANAATG 480
DB 421 YKVAALAEEDGATGRNIVLALEEPYQIALNNGVSGVYIDKKSPAGTGFANAATG 480
QY 481 EYVDIKTKIIDPVKATVRSALONNASSVALITTEAVANKPEPATPAMPAMDPMGM 540
DB 481 EYVNMIDGIVDPKATVRSALONNASSVALITTEAVANKPEPATPAMPAMDPMGM 540
QY 541 GKGCG 545
DB 536 GKGCG 540

RESULT 4
CH60_BACST STANDARD; PRT: 539 AA.
ID CH60_BACST
AC 007201;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 60 kDa chaperonin (protein Cpn60) (groEL protein).
GN GROEL OR GROEL OR LMO2068.
OS Bacteria; Firmicutes; Bacillales; Geobacillus.
OX NCBI_TaxID=1422;

RP SEQUENCE FROM N.A.
RC STRAIN-NDS36;
RX MEDLINE-93224474; PubMed-8096841;
RA Schoen U., Schumann W.;
RT "Molecular cloning, sequencing, and transcriptional analysis of the
RL J. Bacteriol. 175:2465-2469(1993).
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC -1- 7 SUBUNITS (BY SIMILARITY).
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

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 DR EMBL: L10132; AAA2752.1; -
 DR HSP: P06339; IGR1.
 DR InterPro: IPR001844; ChaprinIn_Cpn60.
 DR InterPro: IPR002423; Cpn60/TC-1.
 DR Pfam: PF00118; Cpn60_TCPI.1.
 DR PRINTS: PR00298; CHAPERONIN60.
 DR PRINTS: PR00304; TCMPLEXTCPI.
 DR PROSITE: PS00296; CHAPERONINS_CPN60.1.
 DR Chaperone: ATP-binding; Heat shock.
 KW Chaperone: 539 AA; 57244 MW; 37FE4A0D7492C3E CRC64;
 SQ
 Query Match 76.1%; Score 2026.5; DB 1; Length 539;
 Best Local Similarity 75.0%; Pred. No. 1.8e-86;
 Matches 409; Conservative 63; Mismatches 64; Indels 9; Gaps 2;
 OY 1 MAKEIFSDARAAVGVMDLADTVKTLGPKGRNVLEKAFSGPLITNDGVTIAKEIE 60
 DB 1 MAKEIFSEARARMRGVDLADAVKVLGPKGRNVLEKFGSPILITNDGVTIAKEIE 60
 OY 61 LEDPENNAGALVSEVASKTNDIAGDGTATVLTQAVHSGLNVTAGANPIRGIE 120
 DB 61 LEDPENNAGALVSEVASKTNDIAGDGTATVLTQAVHSGLNVTAGANPIRGIE 120
 OY 121 TATATVETALKAIAOPVSGKEIAIOVAANVSSSEKVEYISSEMERVGNQVITTEESRG 180
 DB 121 TATATVETALKAIAOPVSGKEIAIOVAANVSSSEKVEYISSEMERVGNQVITTEESRG 180
 OY 121 KAVATAIEELAKISKPIQKESIAQVAISADDEVGGLIAEMERVGNQVITTEESRG 180
 OY 181 METELEVEGKQDGRGLISQIWTNDENKVADELNPFLITDKVSNIDILPLEEVK 240
 DB 181 FATELDVEGKQDGRGLISQIWTNDENKVADELNPFLITDKVSNIDILPLEEVK 240
 OY 241 TNRPLITADVDGEALPTLVNKRGTENNVAVAPGQDRKALMEDIALITGCVIT 300
 DB 241 TNRPLITADVDGEALPTLVNKRGTENNVAVAPGQDRKALMEDIALITGCVIT 300
 OY 241 OGPHLLIAEDVEBEAATIVLNKRGTENNVAVAPGQDRKALMEDIALITGCVIT 300
 DB 241 OGPHLLIAEDVEBEAATIVLNKRGTENNVAVAPGQDRKALMEDIALITGCVIT 300
 OY 301 EDGLKDATMTALGOAKITVDKSTVYVSGSSSEAIANRILALIKSOLETTSDR 360
 DB 301 EDGLKDATMTALGOAKITVDKSTVYVSGSSSEAIANRILALIKSOLETTSDR 360
 OY 301 EELGRELKATIASLGRASKVVTKEWTIVGAGDSRIKARINQIRAOLETTSEDR 360
 DB 301 EELGRELKATIASLGRASKVVTKEWTIVGAGDSRIKARINQIRAOLETTSEDR 360
 OY 361 EKLOERLAKLAGVAIVKYGAPETALKEKRLIEDALNSTRAAVEGIVAGGTALMV 420
 DB 361 EKLOERLAKLAGVAIVKYGAPETALKEKRLIEDALNSTRAAVEGIVAGGTALMV 420
 OY 421 IERVALELGDGATGRNIVRALEEPYQIALNAGVSGSVIDIKKSPAGCGFNAAG 480
 DB 421 IERVALELGDGATGRNIVRALEEPYQIALNAGVSGSVIDIKKSPAGCGFNAAG 480
 OY 481 EYVDNKTGIIIDPVKVTNSALONAAVSLITTEAVYANKPEPATPAPAMPDPM- 539
 DB 481 EYVDNKTGIIIDPVKVTNSALONAAVSLITTEAVYANKPEPATPAPAMPDPM- 539
 OY 540 -MGSM 543
 DB 540 -MGSM 543
 OY 534 DMGSM 538
 DB 534 DMGSM 538
 RESULT 5
 CH60_LISTIN STANDARD: PRT: 542 AA.
 AC Q929V0;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).

GN GROEL OR GROEL OR LIN2174.
 OS Listeria innocua.
 OC Bacteria: Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CM11262 / Serovar 6a;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaeser P., Frangeul L., Buchrieser C., Rusnak C., Amend A.,
 RA Baquero F., Berche P., Blocker H., Brandt P., Chakraborty T.,
 RA Charbit A., Chehouani F., Couve E., de Daruvar A., Deboux P.,
 RA Domnan E., Dominguez-Bernal G., Duchaud E., Durant L., Dussauguet O.,
 RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunat F., Kurapkat G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT Comparative genomics of Listeria species.";
 RL Science 294:849-852(2001).
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
 CC CONDITIONS (BY SIMILARITY).
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
 CC 7 SUBUNITS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY!
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AL596171; CAC97403.1; -
 DR L10132; L102174; -
 DR InterPro: IPR001844; ChaprinIn_Cpn60.
 DR InterPro: IPR002423; Cpn60/TCPI-1.
 DR Pfam: PF00118; Cpn60_TCPI.1.
 DR PROSITE: PS00296; CHAPERONINS_CPN60.1.
 DR Chaperone: ATP-binding; Complete proteome.
 KW Chaperone: 542 AA; 57301 MW; 68D6AD2A730DB709 CRC64;
 SQ
 Query Match 76.1%; Score 2026.5; DB 1; Length 542;
 Best Local Similarity 75.0%; Pred. No. 1.8e-86;
 Matches 409; Conservative 62; Mismatches 69; Indels 5; Gaps 2;
 OY 1 MAKEIFSDARAAVGVMDLADTVKTLGPKGRNVLEKAFSGPLITNDGVTIAKEIE 60
 DB 1 MAKEIFSEARARMRGVDLADAVKVLGPKGRNVLEKFGSPILITNDGVTIAKEIE 60
 OY 61 LEDPENNAGALVSEVASKTNDIAGDGTATVLTQAVHSGLNVTAGANPIRGIE 120
 DB 61 LEDPENNAGALVSEVASKTNDIAGDGTATVLTQAVHSGLNVTAGANPIRGIE 120
 OY 121 TATATVETALKAIAOPVSGKEIAIOVAANVSSSEKVEYISSEMERVGNQVITTEESRG 180
 DB 121 TATATVETALKAIAOPVSGKEIAIOVAANVSSSEKVEYISSEMERVGNQVITTEESRG 180
 OY 121 KAVATAIEELAKISKPIQKESIAQVAISADDEVGGLIAEMERVGNQVITTEESRG 180
 DB 121 KAVATAIEELAKISKPIQKESIAQVAISADDEVGGLIAEMERVGNQVITTEESRG 180
 OY 181 METELEVEGKQDGRGLISQIWTNDENKVADELNPFLITDKVSNIDILPLEEVK 240
 DB 181 FATELDVEGKQDGRGLISQIWTNDENKVADELNPFLITDKVSNIDILPLEEVK 240
 OY 241 TNRPLITADVDGEALPTLVNKRGTENNVAVAPGQDRKALMEDIALITGCVIT 300
 DB 241 TNRPLITADVDGEALPTLVNKRGTENNVAVAPGQDRKALMEDIALITGCVIT 300
 OY 241 OGPHLLIAEDVEBEAATIVLNKRGTENNVAVAPGQDRKALMEDIALITGCVIT 300
 DB 241 OGPHLLIAEDVEBEAATIVLNKRGTENNVAVAPGQDRKALMEDIALITGCVIT 300
 OY 301 EDGLKDATMTALGOAKITVDKSTVYVSGSSSEAIANRILALIKSOLETTSDR 360
 DB 301 EDGLKDATMTALGOAKITVDKSTVYVSGSSSEAIANRILALIKSOLETTSDR 360

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OY 361 EKLOERLAKIAGVAVIVKAPETALKEKRLIEDALNTRAIVEGIVAGGATLITV 420
DB 361 EKLOERLAKIAGVAVIVKAPETALKEKRLIEDALNTRAIVEGIVAGGATLITV 420
OY 421 IEKVALEEGDDACGRIVYIPALPEPQALNAGRESSVYIDKLKSPAGCFNAATG 480
DB 421 YNKVALEEGDVEGTINIVRSLEEPQALNAGLESSVYERLKEHVAVGGFNAANG 480
OY 481 EMDMKTGIIIDPVKVTYSALQNASVASLITTEAVANKEPAPAPAMPAGMDPGM 540
DB 481 EMDMKTGIIIDPVKVTYSALQNASVASLITTEAVANKEPAPAPAMPAGMDPGM 540
OY 541 GCMGG 545
DB 536 GCMGG 540

RESULT 6
CH60_BACSU
ID CH60_BACSU STANDARD: PRT: 543 AA.
AC P28598: 005526;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Stress protein H5).
GN GROEL OR MOPR OR GROEL.
OS Bacillus subtilis.
OC Bacteria: Firmicutes: Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID:1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92283754; PubMed-1350777;
RA Schmidt A., Schlesswohl M., Voelker U., Hecker M., Schumann W.;
RT "Cloning, sequencing, mapping, and transcriptional analysis of the
RT groEL operon from Bacillus subtilis.";
RL J. Bacteriol. 174:3993-3999(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-168;
RC MEDLINE-92283753; PubMed-1350776;
RA Li M., Wong S.L.;
RT "Cloning and characterization of the groEL operon from Bacillus
RT subtilis.";
RL J. Bacteriol. 174:3981-3992(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-168;
RC MEDLINE-93129552; PubMed-1369494;
RA Tozawa Y., Yoshikawa H., Kawamura F., Itaya M., Takahashi H.;
RT "Isolation and characterization of the groES and groEL genes of
RT Bacillus subtilis Marburg.";
RL Biosci. Biotechnol. Biochem. 56:1995-2002(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN-168 / Marburg;
RC MEDLINE-98116660; PubMed-9455482;
RA Kasahara Y., Nakai S., Ogasawara N., Yata K., Sadale Y.;
RT "Sequence analysis of the groEL-cocA region of the Bacillus subtilis
RT genome, containing the restriction/modification system genes.";
RL DNA Res. 4:335-339(1997).
RN [5]
RP SEQUENCE OF 1-18 FROM N.A.
RX STRAIN-168 / Marburg;
RC MEDLINE-97346038; PubMed-9202461;
RA Sadale Y., Yata K., Fujita K., Segal H., Itaya M., Kasahara Y.,
RA Ogasawara N.;
RT "Nucleotide sequence and analysis of the phoB-trmE-groEL region of
RT the Bacillus subtilis chromosome.";
RL Microbiology 143:1861-1866(1997).
RN [6]
RP SEQUENCE OF 1-30.
RX STRAIN-168 / IS58;
RC MEDLINE-94282319; PubMed-8012595;

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RA Voelker U., Engelmann S., Maul B., Rietdorf S., Voelker A.,
RA Schmidt R., Mach H., Hecker M.;
RT "Analysis of the induction of general stress proteins of Bacillus
RT subtilis.";
RL Microbiology 140:741-752(1994).
RN [7]
RP SEQUENCE OF 1-30.
RX STRAIN-168 / IS58;
RC MEDLINE-93123969; PubMed-1362210;
RA Voelker U., Mach H., Schmidt R., Hecker M.;
RT "Stress proteins and cross-protection by heat shock and salt stress
RT in Bacillus subtilis.";
RL J. Gen. Microbiol. 138:2125-2135(1992).
CC CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CC CONDITIONS (BY SIMILARITY).
CC CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC CC 7 SUBUNITS (BY SIMILARITY).
CC CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC CC
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DR EMBL: M84965; AAA22531.1;
DR EMBL: M81332; AAA22503.1;
DR EMBL: D10972; BAA22519.1;
DR EMBL: AB007637; BAA22747.1;
DR EMBL: D88802; BAA19727.1;
DR EMBL: Z99107; CAB12422.1;
DR PIR: B41884; B41884;
DR PIR: B41885; B41885;
DR PIR: JCI372; JCI372;
DR HSSP: P06139; JGRL.
DR Subtilisin: BGI0423; groL.
DR InterPro: IPR001844; Chaperonin.Cpn60.
DR InterPro: IPR002423; Cpn60/TCP-1.
DR Pfam: PF00118; Cpn60_TCP1.1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PROSITE: PS00304; TCOMPLEXTCP1.
DR Chapterone: ATP-binding; Heat shock; Complete proteome.
KW INIT_MER
FT INIT_MER 0
FT CONFLICT 14 14 M -> N (IN REF. 3).
FT CONFLICT 124 124 V -> L (IN REF. 3).
FT CONFLICT 201 201 M -> L (IN REF. 3).
FT CONFLICT 374 374 A -> R (IN REF. 3).
SQ SEQUENCE 543 AA; 57293 MW; 587259578FF3800 CRC64;

Query Match 75.9%; Score 2021.5; DB 1; Length 543;
Best Local Similarity 73.7%; Pred. No. 3e-65;
Matches 401; Conservative 69; Mismatches 71; Indels 3; Gaps 1;

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Query	Subject	Score	75.88	Score 2017.5	DB 1	Length 544		
DR	EMBL: AP001508; BAB04281.1; -							
DR	HSSP: P06139; 1GRL							
DR	InterPro: IPR001844; Chaplin.Cpn60.							
DR	InterPro: IPR002423; Cpn60.TCP-1.							
DR	Pfam: PF00118; Cpn60.TCP1.1.							
DR	PRINTS: PR00298; CHAPERONIN60.							
DR	PRINTS: PR00304; TCOMPLEXCP1.							
DR	PROSITE: PS00296; CHAPERONIN.CPN60.1.							
DR	Chaperone: ATP-binding; Heat shock; Complete proteome.							
KM	CONFLICT 407 407							
FT	CONFLICT 421 421							
FT	CONFLICT 500 500							
FT	CONFLICT 512 512							
SO	SEQUENCE 544 AA: 57403 MW: C795E081C903C971 CMC64; *							
Query Match	Best Local Similarity	75.88	Score 2017.5	DB 1	Length 544			
Matches 400	Conservative	74	Mismatches 68	Indels 3	Gaps 1			
OY	1 MAKEIKESADARAARVGVMDLADIVKVTGLSPKGRNVLEKFGSPILITNDGVTIAKIE 60							
DB	1 MAKDIKSESEARSRMSRGVCDKLDAVKVTLSPKGRNVLEKFGSPILITNDGVTIAKIE 60							
OY	61 LEDHEENMGAKLTVSEVASKTNDIADGDTTATVTLQAIHEELKKWAVAGANPGRRIE 120							
DB	61 LEDAEENMGAKLTVAEVASKTNDIADGDTTATVTLQAIMREGLKMTVSGANPWVIRKIE 120							
OY	121 TATATAEALKAIAQPVSGKEALIAOVAASSRSKSGEYISPMERGVNGCVTTEESRG 180							
DB	121 KATQVAEELSKISKPIEGKDSIAQVAAMISSADEGVGKIIAMERGVNGCVTTEESRG 180							
OY	181 MTELEVEVEGNOPDGYLSQWYTDNEKKVADLENPLITIDTKVSNIDIIPLLEEVK 240							
DB	181 FSTELEVEVEGNODRGVNASPMTSDCKEAVLNDPNVLIITDKINSINQVLPVEQVQ 240							
OY	241 TTRPILIIADVDGALPTLVKIKNGFNPNVAVKAPGRGPRRAMEDAIITGTYIT 300							
DB	241 GCKPILIIADVDGALATLVKIKNGFNPNVAVKAPGRGPRRAMEDAIITGTYIT 300							
OY	301 EDLGLKDKATMTALGOAKITTDKRSYIVYEGSGSEAIANRIALKSLETTSDPR 360							
DB	301 EDLGLDKANSITTOGRASKVYTKENTIVYEGSGSDAIARNOAKOIEETTSDDK 360							
OY	361 EKLDEBLAKAGVAVIVNGAPETALKEKMLRIEDALNATRAAVEGVIAGGATLTV 420							
DB	361 EKLDEBLAKAGVAVLVNGAMLETBMERKLRIEDALNSTAAVEGVIAGGATLTV 420							
OY	421 IEKVALELEDGDATGRNIVLRALEBPVROTALNAGYEGSVIIDLKNSPAGTGFNA 480							
DB	421 IKAVSISGGAGEAGVIVLRALEBPVROTAHNAQLDEGVIYERLKKEDAGFGFNATG 480							
OY	481 EYVDIMTGTIDPVKVRSAALQNAASVSLITTEAVVANKPEPATAPAPAGNDPDM 540							
DB	481 EYVNVNENGIVDPTKVRSAALQNAASVAMLTTEAVIADKRENEGGGMP--DMGM 537							
OY	541 GGNG 545							
DB	538 GGNG 542							
RESULT 8								
CH60_BACP3								
ID	CH60_BACP3	STANDARD:	PRT:	538 AA.				
AC	P26209.							
DT	01-MAY-1992 (Rel. 22, Created)							
DT	01-MAY-1992 (Rel. 22, Last sequence update)							
DT	16-OCT-2001 (Rel. 40, Last annotation update)							
DE	60 kDa chaparrin (protein Cpn60) (groEL protein) (Heat shock 61 kDa protein)							
DE	GROEL OR MOPR OR GROEL.							
OS	Bacillus PS3 (Thermophilic bacterium PS-3).							
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.							
OX	NCBI_Taxid:70306;							

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91354309; PubMed-1679330;
 RA Tamada H., Ohta T., Hamamoto T., Ohtawara-Hamamoto Y., Yanagi M.,
 RA Hiratawa H., Hirata H., Kagawa Y.,
 RT *Gene structure of heat shock proteins 61kDa and 12kDa (thermophilic
 RT chaperonins) of thermophilic bacterium P31.
 RL Biochem Biophys Res Commun. 193:565-571(1991).
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
 CC CONDITIONS (BY SIMILARITY).
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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 CC
 DR EMBL: S57424; AAB2915.2; ALT_SEQ.
 DR PIR: J01195; J01195.
 DR HSP: P06139; IGRU.
 DR InterPro: IPR001844; Chaperln_Cpn60.
 DR InterPro: IPR002423; Cpn60/TCF-1.
 DR Pfam: PF00118; Cpn60_TCF1; 1.
 DR PRINTS: PRO0298; CHAPERONIN60.
 DR PRINTS: PRO0304; TCOMPLEXTCPI.
 DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
 KM Chaperone: ATP-binding; Heat shock.
 SQ SEQUENCE 538 AA; 57182 MW; 516C97ACBA227103 CRC64;

Query Match 74.4%; Score 1981; DB 1; Length 538;
 Best Local Similarity 73.7%; Pred. No. 2,2e+8;

Matches 400; Conservative 64; Mismatches 73; Indels 6; Gaps 1;

Oy 1 MAKEIKSADARAAMRGVDMADVYTLGPRGRNVYLEKAFSPITNDGVYTAKEIE 60
 Db 1 MAKQIFSEBARMLRGVLDKADAVKYLGPGRNVYLEKAFSPITNDGVYTAKEIE 60
 Oy 61 LEDHFNMGAKLVSEVASTNDIAGDGTATVTLQAIYHEGLKNVYAGANPIGIRGIE 120
 Db 61 LEDHFNMGAKLVSEVASTNDIAGDGTATVTLQAIYHEGLKNVYAGANPIGIRGIE 120
 Oy 61 LEDHFNMGAKLVSEVASTNDIAGDGTATVTLQAIYHEGLKNVYAGANPIGIRGIE 120
 Db 61 LEDHFNMGAKLVSEVASTNDIAGDGTATVTLQAIYHEGLKNVYAGANPIGIRGIE 120
 Oy 121 TATATAVEALKAIAPVSGKEAIAQVAVSSRSSEKVEYISEAMERYGNDGVYITEESRG 180
 Db 121 KAVAAVAVELKAIKSKPKESIAQVAVSSRSSEKVEYISEAMERYGNDGVYITEESRG 180
 Oy 181 METELEVEVGMQFDGYSQVWYTDNKKVADLENPFILITDKVSNIDILPLEVEVLK 240
 Db 181 FTELEVEVGMQFDGYSQVWYTDNKKVADLENPFILITDKVSNIDILPLEVEVLK 240
 Oy 241 TNRPLLIADVDGALPTVLNKRIGTFNVVAVAPGGRKAMLEIDAILTGTVIT 300
 Db 241 TNRPLLIADVDGALPTVLNKRIGTFNVVAVAPGGRKAMLEIDAILTGTVIT 300
 Oy 241 OGRPLLIADVEGEALATLVNKRIGTFNVVAVAPGGRKAMLEIDAILTGTVIS 300
 Db 241 OGRPLLIADVEGEALATLVNKRIGTFNVVAVAPGGRKAMLEIDAILTGTVIS 300
 Oy 301 EDGLGLKDATMTALGOAKIYVDKSTVYVEGSSSEAIKRNALIKSOLTTSPDFR 360
 Db 301 EDGLGLKDATMTALGOAKIYVDKSTVYVEGSSSEAIKRNALIKSOLTTSPDFR 360
 Oy 301 EELGRELKSTIASLGSRASKVYTKETTTIVBAGDSKRIKAIINQIRAKLETTSEDFR 360
 Db 301 EELGRELKSTIASLGSRASKVYTKETTTIVBAGDSKRIKAIINQIRAKLETTSEDFR 360
 Oy 361 EKIOERLAKLAGVYAYKYGATETALKEKKLIEDALNATRAAVEGIVAGGATLTV 420
 Db 361 EKIOERLAKLAGVYAYKYGATETALKEKKLIEDALNATRAAVEGIVAGGATLTV 420
 Oy 421 IEKVALELEGGDATGRNITVLALEEPYROIALNMGYSGSVYIDKLKNSPAGTFNATG 480
 Db 421 IEKVALELEGGDATGRNITVLALEEPYROIALNMGYSGSVYIDKLKNSPAGTFNATG 480
 Oy 481 EWDIMKTGIIIDPKVYTSALONASVASLITTEVAVNPPEATPAPAMPAGMDGGM 540
 Db 481 EWDIMKTGIIIDPKVYTSALONASVASLITTEVAVNPPEATPAPAMPAGMDGGM 540

Db 481 EWDIMKTGIIIDPKVYTSALONASVASLITTEVAVNPPEATPAPAMPAGMDGGM 540
 Oy 541 GGM 543
 Db 535 GGM 537
 RESULT 9
 CH60_LACHE
 ID CH60_LACHE STANDARD: PRT: 540 AA.
 AC 068324;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).
 GN GROEL OR MOA OR GROEL.
 OS Lactobacillus helveticus.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 CX NCBI_TaxID=1587;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-LH212;
 RX MEDLINE-98439363; PubMed-9766226;
 RA Broadbent J.R., Oberg C.J., Wel L.;
 RT *Characterization of the Lactobacillus helveticus groEL operon.*;
 RL Res. Microbiol. 149:247-253(1998).
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
 CC CONDITIONS (BY SIMILARITY).
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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 CC
 DR EMBL: AF031929; AAC29004.1; .
 DR HSP: P06139; IGRU.
 DR InterPro: IPR001844; Chaperln_Cpn60.
 DR InterPro: IPR002423; Cpn60/TCF-1.
 DR Pfam: PF00118; Cpn60_TCF1; 1.
 DR PRINTS: PRO0298; CHAPERONIN60.
 DR PRINTS: PRO0304; TCOMPLEXTCPI.
 DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
 KM Chaperone: ATP-binding.
 SQ SEQUENCE 540 AA; 57638 MW; 42570DB45FC7C4B4 CRC64;

Query Match 70.5%; Score 1877.5; DB 1; Length 540;
 Best Local Similarity 70.5%; Pred. No. 1,2e+79;
 Matches 382; Conservative 68; Mismatches 87; Indels 5; Gaps 3;

Oy 1 MAKEIKSADARAAMRGVDMADVYTLGPRGRNVYLEKAFSPITNDGVYTAKEIE 60
 Db 1 MAKQIFSEBARMLRGVLDKADAVKYLGPGRNVYLEKAFSPITNDGVYTAKEIE 60
 Oy 61 LEDHFNMGAKLVSEVASTNDIAGDGTATVTLQAIYHEGLKNVYAGANPIGIRGIE 120
 Db 61 LEDHFNMGAKLVSEVASTNDIAGDGTATVTLQAIYHEGLKNVYAGANPIGIRGIE 120
 Oy 121 TATATAVEALKAIAPVSGKEAIAQVAVSSRSSEKVEYISEAMERYGNDGVYITEESRG 180
 Db 121 KAVAAVAVELKAIKSKPKESIAQVAVSSRSSEKVEYISEAMERYGNDGVYITEESRG 180
 Oy 181 METELEVEVGMQFDGYSQVWYTDNKKVADLENPFILITDKVSNIDILPLEVEVLK 240
 Db 181 FTELEVEVGMQFDGYSQVWYTDNKKVADLENPFILITDKVSNIDILPLEVEVLK 240

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OY 241 TNRPLLIADVDGALPTLVNKRNGTENVVAVAKGFGDRKRMEDIALITGGTIT 300
DB 241 OGRSLIADITGEALPTLVNKRNGTENVVAVAKGFGDRKRMEDIALITGGTIT 300
OY 301 EDGLLEKDATATGALGQAATITVDKSTIVYEGSSSEAIANRILISQLETTSDPFR 360
DB 301 EDGLLEKDATATGALGQAATITVDKSTIVYEGSSSEAIANRILISQLETTSDPFR 360
OY 361 EKLOERLAKTAGAVAVIKGAPETALKEKMRLEDLNTNRAVEEIVAGGTTALIV 420
DB 361 EKLOERLAKTAGAVAVIKGAPETALKEKMRLEDLNTNRAVEEIVAGGTTALIV 420
OY 421 IEKVAALEEG---DQATGRNIVFALPEPVROTALNAGSSEVIDKLNKSPAGTGFNA 477
DB 421 -EK-AVEVAGETDEBTGGINIVYRALSPVQALNENAGDSVILDLKLEHGENEIGINA 478
OY 478 AGGEMVMTITGIDPVKVTTSALQNAASVSLITTEAVVANKPEPATPAPMAGNDP 537
DB 478 AKDKENKAVDAGITIDPTVTRTALQNAASVSLITTEAVVANKPEPATPAPMAGNDP 538
OY 538 GM 539
DB 539 GM 540

RESULT 10
CH60_STAAU STANDARD: PRT: 538 AA.
AC P48218:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Heat shock protein 60).
GN GROU. OR MOP. OR GROEL OR HSP60.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9759.
RA COH S.H., Wood J., Hemmingsen S., Chow A.W.;
RL Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U13618; AAA2134.1; -
DR HSSP: P06139; IGRU.
DR InterPro: IPR001844; Chaprnln_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP-1.
DR Pfam: PF00118; Cpn60_TCP1_1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTC1.
DR PROSITE: PS00296; CHAPERONINS_CPN60_1.
KW Chaperone; ATP-binding; Heat shock.
FT INITMET 0 BY SIMILARITY.
SQ SEQUENCE 538 AA; 57518 MW; 8DAAEA9A62446C8E6 CRC64;
Query Match 69.8%; Score 1857.5; DB 1; Length 538;
Best Local Similarity 67.3%; Pred. No. 1e-78;

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Matches 363; Conservative 87; Mismatches 88; Indels 1; Gaps 1;
OY 2 AKIKFSADAAAVGVMLADPVYKTLGPKRNVLEKAFSGPLITIDGTTAKTEL 61
DB 1 AKIKFSADAAAVGVMLADPVYKTLGPKRNVLEKAFSGPLITIDGTTAKTEL 60
OY 62 EDIFENKAKVSVASKNDIADGGTTATVLTQAIYIEGKKNVTAGNPICRIET 121
DB 61 EDIFENKAKVSVASKNDIADGGTTATVLTQAIYIEGKKNVTAGNPICRIET 120
OY 122 ATFAVEALKAIAPVSGKEALAOVAASVSRSEKVEYISSEMERVNDGVITTEESRGM 181
DB 121 AVOVALEHIEISCKVENKNEALQVAISADEIGRISSEMDKNGNDGVITTEESNGF 180
OY 182 ETELEVGMQFRCYLSQYMTDNKRVADLENPFILITDKKVNIDILPLEEVLKT 241
DB 181 NTELEVAGMCFQGYQSPYVWTDKMIIELEPILVTDKRISSFODILPLEEYVQA 240
OY 242 NREPLIADVDGALPTLVNKRNGTENVVAVAKGFGDRKRMEDIALITGGTITE 301
DB 241 SREPLIADVDGALPTLVNKRNGTENVVAVAKGFGDRKRMEDIALITGGTITE 300
OY 302 DGLLEKDATATGALGQAATITVDKSTIVYEGSSSEAIANRILISQLETTSDPFR 361
DB 301 DGLLEKDATATGALGQAATITVDKSTIVYEGSSSEAIANRILISQLETTSDPFR 360
OY 362 EKLOERLAKTAGAVAVIKGAPETALKEKMRLEDLNTNRAVEEIVAGGTTALIV 421
DB 361 EKLOERLAKTAGAVAVIKGAPETALKEKMRLEDLNTNRAVEEIVAGGTTALIV 420
OY 421 IEKVAALEEGDDATGNNIVYRALPEPVROTALNAGSSEVIDKLNKSPAGTGFNA 481
DB 421 QKSELEKAGSVEGVNIVYRALPEPVROTALNAGSSEVIDKLNKSPAGTGFNA 480
OY 482 WDMIKTGIIDPVKVTTSALQNAASVSLITTEAVVANKPEPATPAPMAGNDP 540
DB 481 WDMLEEGIDPTVTRTALQNAASVSLITTEAVVANKPEPATPAPMAGNDP 538

RESULT 11
CH60_STAAU STANDARD: PRT: 538 AA.
AC Q08854;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Heat shock protein 60).
GN GROU. OR MOP. OR GROEL OR HSP60.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
RC STRAIN=912;
RA MEDLINE-93290669; PubMed-7916607;
RX Ohta T., Honda K., Kuroda M., Saito K., Hayashi H.;
RL Molecular characterization of the gene operon of heat shock proteins
RT HSP60 and HSP10 in methicillin-resistant Staphylococcus aureus.
RT Biochem. Biophys. Res. Commun. 193:730-737(1993).
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REPRODING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC -----
DR EMBL: D14711; BAA03533.1;
DR PIR: JN0601; JN0601.
DR HSSP: P06139; 1GRU.
DR InterPro: IPR001844; Chaperonin_Cpn60.
DR InterPro: IPR002423; Cpn60/TCP-1.
DR Pfam: PF00118; Cpn60_TCP1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
DR Chaperone: ATP-binding; Heat shock.
FM INIT_MET 0
FT SEQUENCE 538 AA; 5722 MW; 58173E21AEALCSE CRC64;

Query Match 69.2%; Score 1842.5; DB 1; Length 538;
Best Local Similarity 68.4%; Pred. No. 4.9e-78;
Matches 370; Conservative 78; Mismatches 86; Indels 7; Gaps 4;

OY 3 KEIKTSADARAARVGVDMADLVYKVLGKGNVYLEKAGSPILITNDGVTAKETLE 62
DB 2 KQKTSFEDRQMLRGVDOLANAVYIGRGKNVYLEKFTAPLITNDGVTAKETLE 61
OY 63 DHEENNGAKLYSEVASKTNDIAGDGTATATVLTQAIHVEGLKNVYAGNPIGIRGIETA 122
DB 62 DPEYNNGAKLYQEVANKTNEINGDGTATATVLAQMIQEGKNTVSGANPVGLRGIDKA 121
OY 123 TATAVEALKAIAPVSGKEAIAOVAVSSRSKEVGEYISEMERNVNDGV--ITIEESR 179
DB 122 VKVAVEALHENSOKVENKNEINOVGAISADEEIGYISEATEVENVNDGVITITIEESN 181
OY 180 GMELEVEVGMOFDRGYLSQYVNTDNKKVADLENPILITTDKKSNIODITPLEEVY 239
DB 182 RLNTLELEL--GMQFDRGYOSPWTVDSDKNVLELSPYILVTDKKSISODITPLEEQVY 239
OY 240 KTRNPLLIADVDGALPTLVKIRGTFFNVYAKAFGDRRKMLEDIAITLGTGYT 299
DB 240 QSNRPILIVADEVGSALNTLVLRMGSTPTAAVAKAGFDRRKMLEDIAITLGTGOVY 299
OY 300 TEDLGLKDAKMTALGOAKATYDKDSYIYVGGSSSEAIANRILIKSOLETTTSDDE 359
DB 300 TDDGLDLKDSIDMLGTASKVEYTKDNTVVDGSDGSDNSIDARVSOLKSQTEETSDDE 359
OY 360 REKLOERLAKIAGVAVIVGAPETALKEKMLRIEDALNATRAAVEGIVAGGTALIT 419
DB 360 REKLOERLAKIAGVAVIVGASSETELKERKRIEDALNSTRAAVEGIVAGGTALV 419
OY 420 VIEKVALELEGGDATTGRNIVLRALPEPVROIALNAGYEGSYIDILKISPDAGTFAN 479
DB 420 VYQKSENEAECDIETGVAVILKALTPAVYQIAENAGLEGSIVERTLKNAPRGVNGAT 479
OY 480 GEMVDMITGIIDPVKVTSAIQNAASVASLITIEAVVANKREPTAPAPAMPKMPDG 539
DB 480 NEMVNMRLRGIVDPKVTBSALQHRASVAMFETTEAVVASIFEKKNQPMN--GGM--PGM 537
OY 540 M 540
DB 538 M 538

RESULT 12
CH60_CLOTM STANDARD: PRT: 540 AA.
AC P48212.
DR 01-FEB-1996 (Rel. 33; Created)
DR 01-OCT-1996 (Rel. 34; Last sequence update)
DR 16-OCT-2001 (Rel. 40; Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (HSP-60).
GN GROL OR MOPA OR GROL.
OS Clostridium thermocellum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

CC Clostridium
OX NCBI_TaxID=1515;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-NCIB 10682;
RA MEDLINE=97199381; PubMed=9047357;
RA Ciriela A., Cross S., Freedman R.B., Hazlewood G.P.;
RT "Sequence and transcriptional analysis of groES and groEL genes from
RL the thermophilic bacterium Clostridium thermocellum.";
RL Gene 186:143-147(1997).
RP SEQUENCE OF 1-20.
RC STRAIN-NCIB 10682.
RX MEDLINE=9625758; PubMed=8687408;
RA Cross S.U., Ciriela A., Pomputsa K., Romaniec M.P.M., Freedman R.B.;
RL "Thermotable chaperonin from Clostridium thermocellum.";
RL Biochem. J. 316:615-622(1996).
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS.
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC or send an email to license@lsb-sdb.ch).
DR EMBL: Z68137; CA9242.1;
DR HSSP: P06139; 1GRU.
DR InterPro: IPR001844; Chaperonin_Cpn60.
DR InterPro: IPR002423; Cpn60/TCP-1.
DR Pfam: PF00118; Cpn60_TCP1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
KW Chaperone; ATP-binding.
FM INIT_MET 0
FT CONFLICT 14 15 LE -> ML (IN REF. 2).
FT CONFLICT 20 20 Q -> K (IN REF. 2).
FT SEQUENCE 540 AA; 57343 MW; A638C71A2675C596 CRC64;

Query Match 68.9%; Score 1833.5; DB 1; Length 540;
Best Local Similarity 68.4%; Pred. No. 1.3e-77;
Matches 372; Conservative 77; Mismatches 88; Indels 7; Gaps 2;

OY 2 AKETKSADARAARVGVDMADLVYKVLGKGNVYLEKAGSPILITNDGVTAKETLE 61
DB 1 AKQKTSFEDRQMLRGVDOLANAVYIGRGKNVYLEKFTAPLITNDGVTAKETLE 60
OY 62 DHEENNGAKLYSEVASKTNDIAGDGTATATVLTQAIHVEGLKNVYAGNPIGIRGIET 121
DB 61 DPEYNNGAKLYQEVANKTNEINGDGTATATVLAQMIQEGKNTVSGANPVGLRGIDKA 120
OY 122 TATAVEALKAIAPVSGKEAIAOVAVSSRSKEVGEYISEMERNVNDGVITITIEESR 179
DB 121 AVDAVAEGIKELISQVKNVGEDIAVASISANDEVIDELADAMEKVTNDGVITVEEATM 180
OY 182 ETELEVEVGMOFDRGYLSQYVNTDNKKVADLENPILITTDKKSNIODITPLEEVYKT 241
DB 181 CTNLEIVEGMOFDRGYVSPWVTDEKMEAVLEDPYILITTDKKSNIODITPLEEQVQ 240
OY 242 NRPLLIADVDGALPTLVKIRGTFFNVYAKAFGDRRKMLEDIAITLGTGYTTE 301
DB 241 GKRLVLIADVDGALPTLVKIRGTFTCAVAKAFGDRRKMLEDIAITLGTGOVITS 300
OY 302 DLGLLEKDAKMTALGOAKATYDKDSYIYVGGSSSEAIANRILIKSOLETTTSDDE 361
DB 301 DLGLLEKDAKMTALGOAKATYDKDSYIYVGGSSSEAIANRILIKSOLETTTSDDE 360

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Oy 362 KLEERLAKLGGVAVIRKVAAPTETALKEKRIEDALNTRAIVEGIVAGGTALITVI 421
Db 361 KLEERLAKLGGVAVIRKVAAPTETALKEKRIEDALNTRAIVEGIVAGGTALITVI 420
Oy 422 EKVAAAL--ELEGGDATTGRNIVLRALPEEPROJALNAGYEGSVYIKLNSPAGTGNAT 479
Db 421 PVAIVADTVTSGDEKTVGOVITLRALPEEPROJALNAGYEGSVYIKLNSPAGTGNAT 480
Oy 480 GEMVDMIKTGIIDPYKTVRSALNAAVSALITTEAVANKPEEPATPAMPAGNDPM 539
Db 481 EKVYVMLEAGTIDPYKTVRSALNAAVSALITTEAVANKPEEPATPAMPAGNDPM 538
Oy 540 MGGM 543
Db 536 MGGM 539

RESULT 13
CH60.CLOPE STANDARD: PRT: 539 AA.
AC P26821.
DT 01-AUG-1992 (Rel. 23, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN GROEL OR MOXA OR GROEL OR CPE2289.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_Taxid:1502;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92182020;
RA Ruengnawana B., Singh B., Gupta R.S.;
RT "Cloning of HSP60 (groEL) operon from Clostridium perfringens using a
RT polymerase chain reaction based approach.";
RL Biochim. Biophys. Acta 1130:90-94(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-13 / Type A;
RA P26821-11792842;
RA Shima T., Ogasawara N., Hattori M., Kuhara S., Yamashita H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC -----
DR EMBL: X62914: CAA44697.1;
DR EMBL: AP003193: BAB81995.1;
DR PIR: S18869: S18869;
DR PIR: S23442: S23442;
DR HSSP: P06139: 1GRL;
DR InterPro: IPR001844: Chaperin_Cpn60;
DR Pfam: PF00118: Cpn60_TCP1;
DR PRINTS: PR00298: CHAPERONIN60;
DR PRINTS: PR00304: TCOMPLEXTCP1;
DR PROSITE: PS00296: CHAPERONIN60_CPN60_1.

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KW Chaperone: ATP-binding; Complete proteome.
FT CONFLICT 344 V -> I (TM REF. 1).
SQ SEQUENCE 539 AA: 57366 MM; E6498C7DD1DE29 CRC64:
Query Match
Best Local Similarity 68.3%; Score 1618; DB 1; Length 539;
Matches 366; Conservative 78; Mismatches 92; Indels 6; Gaps 2;
Oy 1 MAKEIRFADRAAAYRGVMDLADTVKVLGGRKANNVLEKAFSPILINDGVITAKEIE 60
Db 1 MMTLLFGEERKSRMKGVDKLANVTAVVLGGRKANNVLDKFKGSPILINDGVITAREIE 60
Oy 61 LEDHEENKAKLYSEVASKINDIAGDGTATATVLTQAVIHGKLNAGANPIGIRGIE 120
Db 61 LEDAVENKAGOLYKAVATKINDVAGDGTATATVLTQAVIHGKLNAGANPILIRNGIK 120
Oy 121 TATATAVALKAAQVSGKKAIVQAAVSRSEKVEYSEAMERVNDGVITIEESRG 180
Db 121 TAVEKAVEIEIKSKPVNGKEDIRVAALSADEKICGLTADMEKVEYGVITIEESRS 180
Oy 181 METELEVEYEGMGDFRGYLSQYMTNDKKNVADLEMPILITTDKKSNIQDILPLEEYIK 240
Db 181 MGTEDLVYEGMGDFRGYLSQYMTNDKKNVADLEMPILITTDKKSNIQDILPLEEYIQ 240
Oy 241 TTRPLLITADVUGELPLVLYKIKGTNNVAVKAPGCDRRKAMLEDIALITGTVIT 300
Db 241 ACKKLLITADIDIGEMMTLVNKLKGTFCVGAAPGDFDRKREKLEDTITLGTVVIS 300
Oy 301 EDGLLEKDATMTALGOAAKITVDKSTVIVEGSSSEAIANRIALIRSOLETTSDPFR 360
Db 301 DEVGGDKLEATIDLMIGAEASVYKSTTIVNGRNSSEIKNRVNDIKOLEATSTSPDK 360
Oy 361 EKLDERLAKLGGVAVIRKVAAPTETALKEKRIEDALNTRAIVEGIVAGGTALITV 420
Db 361 EKLDERLAKLGGVAVIRKVAAPTETALKEKRIEDALNTRAIVEGIVAGGTALIVAV 420
Oy 421 IEKVAALELE-GDDATGRNIVLRALPEEPROJALNAGYEGSVYIKLNSPAGTGNAT 479
Db 421 INEVAKLSDIQDEQVGINIIVSLEEPROJALNAGYEGSVYIEKVNDSAGIGDALR 480
Oy 480 GEMVDMIKTGIIDPYKTVRSALNAAVSALITTEAVANKPEEPATPAMPAGNDPM 539
Db 481 GEMVDMIKTGIIDPYKTVRSALNAAVSALITTEAVANKPEEPATPAMPAGNDPM 535
Oy 540 MG 541
Db 536 DG 537

RESULT 14
CH60.CLOAB STANDARD: PRT: 543 AA.
AC P30717.
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN GROEL OR MOXA OR GROEL OR CAC2703.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_Taxid:1488;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-ATCC 4259 / DSM 1731 / NCIB 619;
RX MEDLINE-92250424; PubMed-1349602;
RA Netherhaus F., Bahl H.;
RT "Cloning, sequencing, and molecular analysis of the groEL operon of
RT Clostridium acetobutylicum.";
RL J. Bacteriol. 174:3282-3289(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

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RX MEDLINE-21359325; PubMed-11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hittl J., Wolf Y.I.,
RA Talusov R.L., Sabath F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.
RL J. Bacteriol. 183:4823-4838(2001).
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC -----
DR EMBL: M74572; AAA23243.1;
DR EMBL: AE007768; AKK80649.1;
DR PIR: B41872; B41872.
DR HSSP: P06139; 1GRL.
DR InterPro: IPR001844; Chaprin.Cpn60.
DR InterPro: IPR002423; Cpn60/TCF-1.
DR Pfam: PF00118; Cpn60_TCF1.1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCF1.
DR PROSITE: PS00296; CHAPERONIN60.
DR Chaperone: ATP-binding; Complete proteome.
KM SEQUENCE 543 AA; 58073 MW; 6FD16C2EBD0A03DAC CRC64;
SQ
Query Match 66.7%; Score 1776; DB 1; Length 543;
Best Local Similarity 66.3%; Pred. No. 5, se-75;
Matches 362; Conservative 78; Mismatches 100; Indels 6; Gaps 4;
OY 1 MAKEIFSADAAAVRGVMDLADTVKVLGPKGRNVYLEKAGSPILITNDGVTAKREIE 60
DB 1 MAKQILYGEARSRMOKGVLDKADTVKVLGPKGRNVLDKKKGAFLITNDGVSIAKEIE 60
OY 61 LEDHFENMGAKLYSEVASKTNDIADGGTTATVLTQAIYHEGLKAVTAGAPICIRGIE 120
DB 61 LEDPEKMGAGLYKREAVKATKTDVAGDGTITATLQAIYHEGLKAVTAGAPILIRNGIR 120
OY 121 TATATAVEALKAIAQVSGKRAIAQVAASRSSEKVEYISEMERVNDGVITIEESRG 180
DB 121 TATATAVEALKAIAQVSGKRAIAQVAASRSSEKVEYISEMERVNDGVITIEESRG 180
OY 122 LAVDKTYEGLKTVSKNVKNGKEDARVASISADEIKLADMKRVNBEVITVESSS 180
DB 122 LAVDKTYEGLKTVSKNVKNGKEDARVASISADEIKLADMKRVNBEVITVESSS 180
OY 181 METELEVEBQKQFDRGYLSQVWTDNKKVADLBNPELITTKKVSNIQDITLPLEEVK 240
DB 181 MGTELDVEBQKQFDRGYLSQVWTDNKKVADLBNPELITTKKVSNIQDITLPLEEVK 240
OY 241 TNRPLLIADVDGEALPTVYLNKIRNGTFNVAVAKAGFGRKMALEDIAITGGTIVT 300
DB 241 OGKRLIADVDGEALPTVYLNKIRNGTFNVAVAKAGFGRKMALEDIAITGGTIVT 300
OY 301 EDLGLLELDKATWTALGQAKITVDKSTVIEGSGSSEALNRIALILISOLETTSDPR 360
DB 301 EELGLDKLDVKEEDGSAESVSKISKENTIVYNGSGDSAIHNRVAINQOIEETSDPR 360
OY 361 EKLOERLAKAGGAVAVIVGAPTEFLTKEMKRLIEDLNATRAAEETIVAGGTTALIV 420
DB 361 EKLOERLAKAGGAVAVIVGAPTEFLTKEMKRLIEDLNATRAAEETIVAGGTTALIV 420
OY 421 IEKVAALEL-BGDDATGNINYLAALEPPYROIALINAGYEGSVYIDKLKNSPAGTGNAT 479
DB 421 LPEVRELISDEPDDVOVGINTIVKALEEPYROIANAGLESVYIEKRIINSEKIGFDALH 480
OY 480 GEVMDIKTIGIIDPVKTRSAIONAASVASTLITTEAVVANKPEPATPAPAMPAGMDPRM 539

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DB 481 EKVIDMSIGVIDPKVTRSAIONAASVASTLITTECAVADIPE--KDRPEMGGA-EGM 537
OY 540 MGGMG 545
DB 538 --GGMG 541
RESULT 15
CH60_THEBR STANDARD; PRT; 540 AA.
ID CH60_THEBR
AC 060024;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin (protein Cpn60) (groEL protein).
GN GROL OR MOBA OR GROEL
OS Thermanaerobacter brockii (Thermanaerobium brockii).
OC Bacteria; Firmicutes; Clostridia; Thermosphaerobacteriales;
OC Thermosphaerobacteriaceae; Thermosphaerobacter.
OX NCBI_TaxID=29323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RT8_G4.
RX MEDLINE-99014232; PubMed-9795109;
RA Truscott K.N., Scopes R.K.;
RT "Sequence analysis and heterologous expression of the groE genes from
RT Thermosphaerobacter sp. RT8_G4."
RL Gene 217:15-23(1998).
RN [2]
RP SEQUENCE OF 1-43, AND CHARACTERIZATION.
RC STRAIN=RT8_G4.
RX MEDLINE-94291621; PubMed-7912671.
RA Truscott K.N., Hoef P.B., Scopes R.K.;
RT "Purification and characterization of chaperonin 60 and chaperonin 10
RT from the anaerobic thermophile Thermosphaerobacter brockii."
RL Eur. J. Biochem. 222:277-284(1994).
RN [3]
RP -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
RP PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
RP CONDITIONS (BY SIMILARITY).
RP -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
RP 7 SUBUNITS (BY SIMILARITY).
RP -1- MASS SPECTROMETRY: MW=57949; MW-ERR=10; METHOD=Electrospray.
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC -----
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CC -----
DR EMBL: U56021; BAB00559.1;
DR HSSP: P06139; 1GRL.
DR InterPro: IPR001844; Chaprin.Cpn60.
DR InterPro: IPR002423; Cpn60/TCF-1.
DR Pfam: PF00118; Cpn60_TCF1.1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCF1.
DR PROSITE: PS00296; CHAPERONIN60.
DR Chaperone: ATP-binding; Complete proteome.
KM INIT_MET 0
FT INIT_MET 0
FT CONFLICT 43
SQ SEQUENCE 540 AA; 57928 MW; 27C316AD5C61734 CRC64;
Query Match 64.7%; Score 1723.5; DB 1; Length 540;
Best Local Similarity 64.9%; Pred. No. 1, se-72;
Matches 349; Conservative 80; Mismatches 106; Indels 3; Gaps 2;
OY 2 AKETIFSADAAAVRGVMDLADTVKVLGPKGRNVYLEKAGSPILITNDGVTAKREIE 61
DB 1 AKQIKYGEARSRMOKGVLDKADTVKVLGPKGRNVLDKKKGAFLITNDGVTAKREIE 60

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OY 62 EDHEENKALYSEVASTNDIAGDGTATVYTOAIVHEGLKNTAGANPIRGITET 121
DB 61 EDPENOGAGOLKEATKNDIAGDGTATVYTOAIVHEGLKNTAGANPMLRGIAR 120
OY 122 ATATAVALKAIAPVSGKEAIAOVAASNSKEVGEYISEAMERVNDGVITIEESRG 181
DB 121 AVDAVAGLKRISKIDNKESIAHVASISADDEIGLIAEAMDVKGKGVITIEESKTL 180
OY 182 ETELEVVEGMOFDRGYLSOYVWTDNEKVVADLENPFILITDKKVSNIQDILPLEEVLKT 241
DB 181 GTLEVEVEGMOFDRGYLSOYVWTDNEKVVADLENPFILITDKKVSNIQDILPLEEVLKT 240
OY 242 NRPLIADVDGEALPTLVNKRIGCTFNVAVAVKAPGCDRRKAMLEDIAILITGGTYTE 301
DB 241 GKLLIADVDGEALPTLVNKRIGCTFNVAVAVKAPGCDRRKAMLEDIAILITGGTYTE 300
OY 302 DLGELKDATMTALGOAKITVDKOSTYVEGSSSEALANRILIKSOLETTSDPRE 361
DB 301 ELGYDLKDVRLDMGRAROVKTYKEYTIVGAGDSEIKRKNQIKAOLEETSDYDRE 360
OY 362 KLOERLAKIAGVAVIKVAPFTALKEKRLIEDALNTRAVEGIVAGGTALITVI 421
DB 361 KLOERLAKIAGVAVIKVAPFTALKEKRLIEDALNTRAVEGIVAGGTALITVI 420
OY 422 EKVAL--ELEGDATGNTIVLRALEEPVROIALNAGYEGSVIDKLKS-PAGTFNAA 478
DB 421 EDVAKVVDLSLEDGFTAKIVLRALEEPVROIALNAGYEGSVIYERIKAKDPNFGYDAY 480
OY 479 TGEVDMIRKTIIDPVVTRSAIQNNAVASLITTEAVVANKPEPATPAPAMPAGMD 536
DB 481 KEETDMFRAGIVDPFTVTRTALQONNASTMILITTEAVVANKPEPATPAPAMPAGMD 538

Search completed: April 8, 2003, 14:23:41
Job time : 16 secs